
 W P E S E R E H
 (nm)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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MPsrch_dp protein - protein database search, using Smith-Waterman algorithm
 Run on: Sat May 13 08:40:18 2000; MasPar time 4.47 Seconds
 Tabular output not generated. 318.123 Million cell updates/sec

Title: >US-09-331-631-21
 Description: (32-91) from US09331631.pep
 Perfect Score: 453
 Sequence: 1 TENPCAQRCLQSCQDEPDDL.....DTGATNQRHPPERTRGROP 60

Scoring table: PAM 150
 Gap 11

Searched: 188963 segs, 23686106 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: a:geneseq35
 1:geneseqp

Statistics: Mean 24.616; Variance 91.839; scale 0.268

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	453	100.0	614	1	Arachis hypogaea antim	4.98e-39
2	453	100.0	614	1	Peanut allergen Ara hi	4.98e-39
3	396	87.4	626	1	Peanut allergen Ara hi	1.02e-32
4	119	26.3	605	1	Glycine max antinutro	2.44e-03
5	93	20.5	680	1	Human KAL protein.	6.89e-01
6	93	20.5	680	1	Sequence encoded by a	5.48e-00
7	83	18.3	625	1	Macadamia integrifolia	8.24e+00
8	81	17.9	525	1	Theobroma cacao anti	8.24e+00
9	81	17.9	566	1	Sequence encoded by 67	1.84e+01
10	77	17.0	590	1	Gossypium hirsutum ant	1.84e+01
11	77	17.0	666	1	Macadamia integrifolia	1.84e+01
12	77	17.0	666	1	Macadamia integrifolia	1.84e+01
13	75	16.6	149	1	Human insulin receptor	2.74e+01
14	75	16.6	252	1	Protein cognate of pro	2.74e+01
15	74	16.3	683	1	Novel human protein. d	4.06e+01
16	73	16.1	593	1	Zea mays antimicrobial	4.06e+01
17	72	15.9	144	1	H. pylori membrane pro	7.28e+01
18	70	15.5	500	1	Partial rat thrombomod	7.28e+01
19	70	15.5	559	1	Partial rat thrombomod	7.28e+01
20	70	15.5	577	1	Rat thrombomodulin.	7.28e+01
21	70	15.5	956	1	Soluble human insulin	7.28e+01
22	70	15.5	1087	1	B lymphocyte membrane	7.28e+01
23	70	15.5	1370	1	Sequence encoded by hu	7.28e+01

ID	Score	Query Match	Length	ID	Description	Pred. No.
24	70	15.5	1382	1	Wild type human insuli	7.28e+01
25	69	15.2	106	1	Poxvirus ORF-2 truncat	8.83e+01
26	69	15.2	111	1	Poxvirus ORF-2 truncat	8.83e+01
27	69	15.2	116	1	Poxvirus ORF-2 truncat	8.83e+01
28	69	15.2	121	1	Poxvirus ORF-2 truncat	8.83e+01
29	69	15.2	148	1	Poxvirus ORF-2 truncat	8.83e+01
30	69	15.2	148	1	Poxvirus ORF-2 (VEGF r	8.83e+01
31	69	15.2	220	1	HSV-2 strain SB5 Conti	8.83e+01
32	69	15.2	255	1	Human receptor induced	8.83e+01
33	68	15.0	219	1	Human h4-1BBSV recepto	1.07e+02
34	68	15.0	219	1	Human h4-1BBSV recepto	1.07e+02
35	68	15.0	251	1	Malate isomerase sequ	1.07e+02
36	68	15.0	255	1	Human 4-1BB receptor.	1.07e+02
37	68	15.0	255	1	H4-1BB receptor protei	1.07e+02
38	68	15.0	306	1	Amino acid sequence of	1.07e+02
39	68	15.0	306	1	A desaturase enzyme en	1.07e+02
40	68	15.0	306	1	Human desaturase enzym	1.07e+02
41	68	15.0	509	1	Human cyclin D1-human	1.07e+02
42	68	15.0	647	1	Human cyclin D1/cyclin	1.07e+02
43	68	15.0	662	1	Human desaturase enzym	1.07e+02
44	68	15.0	746	1	Human desaturase enzym	1.07e+02
45	68	15.0	746	1	A desaturase enzyme en	1.07e+02

ALIGNMENTS

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23	70	15.5	1370	1	Sequence encoded by hu	7.28e+01

DT 16-APR-1992 (first entry)
DE Sequence encoded by 67 kb T. cacao protein cDNA
KM Cocos; flavour; vitamin; seed storage protein.
OS Theobroma cacao.
PN M09119801-A.
PD 26-DEC-1991.
PF 07-JUN-1991; G00914.

Pt	Roenroek AJM,
Pt	Schaliken JA;
Df	WPI: 87-32896/47.
Ft	Recombinant DNA containing the fur gene - used for producing fibrin protein and antibodies and as a diagnostic aid in the detection of tumours.
Ps	Disclosure: Fig 10; 24pp; English.
Cc	The sequence of the human insulin receptor is provided for comparison with the cysteine-rich region of furin. Furin is strongly expressed in specific types of tumors and labelled RNA or DNA probes of the fur gene and antibodies against furin can be used for diagnostic purposes.
Sc	(See also N70061, N70062, N70060, P70056 and P70058)
Sq	Sequence 149 AA:
Db	Query Match Best Local Similarity 42.9%; Matches 15; Conservative 3; Mismatches 14; Indels 3; Gaps 3
Oy	Score 75; DB 1; Length 149; Pred. No. 2,74e+01; Mismatches 14; Indels 3; Gaps 3
Df	25 CHSECLGNCSQ-PDDPT-K-CVCAARNRYLDGRCV 56
Ig	: : ::
Gz	36 CAQRCLGSCQEPPDLKQGACESRCTKLXPRCV 70
Result	14
ID	WI5773 standard; Protein; 252 AA.
Ac	WI5773;
Dt	31-OCT-1997 (first entry)
De	Protein cognate of protein kinase C-theta (clone #10 product).
Kw	Signal transduction; cell signalling; modulator; immunomodulator;
Rv	human: protein kinase C-beta; PKC-beta; cognate; graft rejection;
Kx	autoimmune disease; allergy; asthma; therapy.
Hr	Homo sapiens.
Ft	Key Location/Qualifiers
Misc_difference	230 /note= "encoded by TAG"
FT	WT MO9714038-AI. 17-APR-1997.
PF	10-OCT-1986; UI6195.
PR	18-JUN-1996; US-665647.
PR	10-OCT-1995; US-541964.
PA	31-JAN-1996; US-594447.
TERR-) TERRAPIN TECHNOLOGIES INC.
PI	Kauvar LM, Mochly-Rosen D, Napoliitano EW, Ron D;
Vasquez NJ, Voronova A;	
N-PSDB:	160588.
Identifying	a modulator of intracellular signal transduction - by determining the interaction of a signal generating peptide with the test substance, allows modulation of the immune system
Example 8:	Fig 15B; 74pp; English.
This sequence	is a protein cognate of protein kinase C-theta (PKC-theta) that binds to theta VI but not to delta VI of lamtin. The amino acid sequence was deduced from cDNA clone #10 (T60588), isolated from a human CD4+ T-cell DNA library using a yeast two-hybrid system. A claimed method for prepn. of the cognate involves culturing recombinant host cells under conditions where the cognate is produced. The cognate is used in a claimed method for identifying modulators of intracellular signal transduction. This involves assessing the ability of candidate modulators to affect the interaction between a catalytically active signal-generating protein (e.g. PKC-theta) and a cognate binding protein involved in modulating the signal transduction function. Substances identified using this method are used to modulate the immune system in a subject (claimed). They act to reduce T-cell activity, reduce the rate of graft rejection, reduce the severity of an autoimmune disorder, ameliorate an allergic and/or asthmatic response, or diminish cytokine response (claimed).
Sq	Sequence 252 AA:
Query Match	16.6% Score 75; DB 1; Length 252;
Best Local Similarity	35.7%; Pred. NO. 2.74e+01;
Matches	10; Conservative 6; Mismatches 10; Indels 2; Gaps 2

Db 62 EHCPLP-CLHGCDKSAATSLKODA-DDMK 87
| : | | : | : | | : | :
Oy 33 ENPCMGROLOSGCQCEPPDLKKKAESNR 60

RESULT 15
ID W36794 standard; Peptide: 683 AA.
AC W36794;
DT 23-APR-1998 (first entry)
DE Novel human protein, designated MWPI, which contains WW domains.
KW Peptide recognition unit; YAP WW domain binding protein; WBP-1; WBP-2;
KW WW domain; cell signalling; growth regulation; cytoskeleton organisation
KM targeted drug screening; modulator; WW domain interaction; MWPI.
OS Homo sapiens.

Key Location/Qualifiers
FT 162..197
FT /note= "WW domain 1"
FT 192..229
FT /note= "WW domain 2"
FT 267..305
FT /note= "WW domain 3"
FT 307..344
FT /note= "WW domain 4"

Domain
Domain
Domain
Domain
Domain

PV W09373723-A1.
PD 09-OCT-1997.
PF 03-APR-1997; U05547.
PR 03-APR-1996; US-630916.
PA (CYTO-) CYTOGEN CORP.
PI (UYNC-) UNIV NORTH CAROLINA.
PI Fowlkes DM, Kay BK, Pitrozzi G;
DR WPI: 97-503234/46.
DR NPSPDB: T95687.
PT Identifying cell signalling and growth regulatory polypeptides by
PT resection with multivalent recognition complex - polypeptides are
PS useful in targeted drug selection
PS Claim 48; Fig 17; 220pp; English.
CC The present sequence represents a novel protein MWPI. The MWPI gene was
CC identified and isolated from human bone marrow and brain cDNA libraries,
CC using peptides W38103-05. These peptide recognition units are based on
CC the sequences of WW domain binding domains of the YAP WW domain binding
CC proteins WBP-1 and WBP-2. The WW domain is a small functional domain
CC found in a large number of proteins from a variety of species including
CC humans, nematodes and yeast. Its name is derived from the observation
CC that two tryptophan residues, one in the amino terminal portion of the
CC WW domain and one in the carboxyl terminal portion, are conserved. Most
CC proteins containing WW domains have a function involving cell signalling
CC and growth regulation or the organisation of the cytoskeleton.
CC Polypeptides containing a WW domain are identified by treating a
CC multivalent recognition unit complex that has selective binding affinity
CC for a WW domain, with many polypeptides and identifying those with
CC selective affinity for the complex. Proteins containing WW domains are
CC used for targeted drug screening, i.e. to identify potential modulators
CC of specific WW domain interactions. The valency of the recognition unit
CC is important in determining specificity of interaction with WW domains.
CC In multivalent form specificity is relaxed, but not lost, so proteins
CC containing WW domains similar, but not identical, to the sequence of the
CC peptides' target WW can be detected, including new polypeptides.
SQ Sequence 683 AA;

Query Match 16.3%; Score 74; DB 1; Length 683;
Best Local Similarity 27.5%; Pred. No. 3.34e+01;
Matches 11; Conservative 14; Mismatches 13; Indels 2; Gaps 2;

Db 104 NECIPSTSAELSEARSLLEDPTSNNSSSAFAEAASROP 143
| : | | : | : | | : | :
Oy 54 KAC-ESRCIKLEDPKCVDIAGNOHHPG-ETRIKROP 91

Search completed: Sat May 13 08:40:26 2000
Job time : 8 secs.

